SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ni, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.

(ii) TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Roseland
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07068

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/467,265
(B) FILING DATE: 06-JUN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Ferraro, Gregory D.
(B) REGISTRATION NUMBER: 36,134
(C) REFERENCE/DOCKET NUMBER: 325800-456

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 201-994-1700
(B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 918 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 31..843

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AAGGGAACGT GTTTCTCCCC TCGTTTGGTC ATG GAG GCG CTG CCC CTG CTA GCC        54
                                 Met Glu Ala Leu Pro Leu Leu Ala
                                   1               5

GCG ACA ACT CCG GAC CAC GGC CGC CAC CGA AGG CTG CTT CTG CTG CCG       102
Ala Thr Thr Pro Asp His Gly Arg His Arg Arg Leu Leu Leu Leu Pro
     10                  15                  20

CTA CTG CTG TTC CTG CTG CCG GCT GGA GCT GTG CAG GGC TGG GAG ACA       150
Leu Leu Leu Phe Leu Leu Pro Ala Gly Ala Val Gln Gly Trp Glu Thr
 25                  30                  35                  40

GAG GAG AGG CCC CGG ACT CGC GAA GAG GAG TGC CAC TTC TAC GCG GGT       198
Glu Glu Arg Pro Arg Thr Arg Glu Glu Glu Cys His Phe Tyr Ala Gly
                 45                  50                  55

GGA CAA GTG TAC CCG GGA GAG GCA TCC CGG GTA TCG GTC GCC GAC CAC       246
Gly Gln Val Tyr Pro Gly Glu Ala Ser Arg Val Ser Val Ala Asp His
             60                  65                  70

TCC CTG CAC CTA AGC AAA GCG AAG ATT TCC AAG CCA GCG CCC TAC TGG       294
Ser Leu His Leu Ser Lys Ala Lys Ile Ser Lys Pro Ala Pro Tyr Trp
         75                  80                  85

GAA GGA ACA GCT GTG ATC GAT GGA GAA TTT AAG GAG CTG AAG TTA ACT       342
Glu Gly Thr Ala Val Ile Asp Gly Glu Phe Lys Glu Leu Lys Leu Thr
     90                  95                 100

GAT TAT CGT GGG AAA TAC TTG GTT TTC TTC TTC TAC CCA CTT GAT TTC       390
Asp Tyr Arg Gly Lys Tyr Leu Val Phe Phe Phe Tyr Pro Leu Asp Phe
105                 110                 115                 120

ACA TTT GTG TGT CCA ACT GAA ATT ATC GCT TTT GGC GAC AGA CTT GAA       438
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Gly Asp Arg Leu Glu
                125                 130                 135

GAA TTC AGA TCT ATA AAT ACT GAA GTG GTA GCA TGC TCT GTT GAT TCA       486
Glu Phe Arg Ser Ile Asn Thr Glu Val Val Ala Cys Ser Val Asp Ser
            140                 145                 150

CAG TTT ACC CAT TTG GCC TGG ATT AAT ACC CCT CGA AGA CAA GGA GGA       534
Gln Phe Thr His Leu Ala Trp Ile Asn Thr Pro Arg Arg Gln Gly Gly
        155                 160                 165

CTT GGG CCA ATA AGG ATT CCA CTT CTT TCA GAT TTG ACC CAT CAG ATC       582
Leu Gly Pro Ile Arg Ile Pro Leu Leu Ser Asp Leu Thr His Gln Ile
    170                 175                 180

TCA AAG GAC TAT GGT GTA TAC CTA GAG GAC TCA GGC CAC ACT CTT AGA       630
Ser Lys Asp Tyr Gly Val Tyr Leu Glu Asp Ser Gly His Thr Leu Arg
185                 190                 195                 200

GGT CTC TTC ATT ATT GAT GAC AAA GGA ATC CTA AGA CAA ATT ACT CTG       678
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Leu
                205                 210                 215
```

```
AAT GAT CTT CCT GTG GGT AGA TCA GTG GAT GAG ACA CTA CGT TTG GTT      726
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
            220                 225                 230

CAA GCA TTC CAG TAC ACT GAC AAA CAC GGA GAA GTC TGC CCT GCT GGC      774
Gln Ala Phe Gln Tyr Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
        235                 240                 245

TGG AAA CCT GGT AGT GAA ACA ATA ATC CCA GAT CCA GCT GGA AAG CTG      822
Trp Lys Pro Gly Ser Glu Thr Ile Ile Pro Asp Pro Ala Gly Lys Leu
    250                 255                 260

AAG TAT TTC GAT AAA CTG AAT TGAGAAATAC TTCTTCAAGT TATGATGCTT         873
Lys Tyr Phe Asp Lys Leu Asn
265                 270

GAAAGTTCTC AATAAAGTTC ACGGTTTCAT TACCACAAAA AAAAA                    918
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Glu Ala Leu Pro Leu Leu Ala Ala Thr Thr Pro Asp His Gly Arg
 1               5                  10                  15

His Arg Arg Leu Leu Leu Leu Pro Leu Leu Leu Phe Leu Leu Pro Ala
            20                  25                  30

Gly Ala Val Gln Gly Trp Glu Thr Glu Glu Arg Pro Arg Thr Arg Glu
        35                  40                  45

Glu Glu Cys His Phe Tyr Ala Gly Gly Gln Val Tyr Pro Gly Glu Ala
    50                  55                  60

Ser Arg Val Ser Val Ala Asp His Ser Leu His Leu Ser Lys Ala Lys
65                  70                  75                  80

Ile Ser Lys Pro Ala Pro Tyr Trp Glu Gly Thr Ala Val Ile Asp Gly
                85                  90                  95

Glu Phe Lys Glu Leu Lys Leu Thr Asp Tyr Arg Gly Lys Tyr Leu Val
            100                 105                 110

Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu Ile
        115                 120                 125

Ile Ala Phe Gly Asp Arg Leu Glu Glu Phe Arg Ser Ile Asn Thr Glu
    130                 135                 140

Val Val Ala Cys Ser Val Asp Ser Gln Phe Thr His Leu Ala Trp Ile
145                 150                 155                 160
```

```
Asn Thr Pro Arg Arg Gln Gly Gly Leu Gly Pro Ile Arg Ile Pro Leu
                  165                 170                 175

Leu Ser Asp Leu Thr His Gln Ile Ser Lys Asp Tyr Gly Val Tyr Leu
              180                 185                 190

Glu Asp Ser Gly His Thr Leu Arg Gly Leu Phe Ile Ile Asp Asp Lys
          195                 200                 205

Gly Ile Leu Arg Gln Ile Thr Leu Asn Asp Leu Pro Val Gly Arg Ser
      210                 215                 220

Val Asp Glu Thr Leu Arg Leu Val Gln Ala Phe Gln Tyr Thr Asp Lys
225                 230                 235                 240

His Gly Glu Val Cys Pro Ala Gly Trp Lys Pro Gly Ser Glu Thr Ile
                  245                 250                 255

Ile Pro Asp Pro Ala Gly Lys Leu Lys Tyr Phe Asp Lys Leu Asn
              260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGCGGATCC ATGGAGGCGC TGCCCTGCT 29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGCCCATGGA GGCGCTGCCC CTG 23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGCCCATGGC TGGAGCTGTG CAGGG 25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCGTCTAGA TCAATTCAGT TTATCGAAAT ACTTCAGC 38

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCGGATCC GCTGGAGCTG TGCAGG 26

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGGATCCC GAGGCGCTGC CCCTGC 26

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGATCCT CAATTCAGTT TATCGAAATA C 31

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA GGCGCTGCCC CTG 33

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGGATCCT CAATTCAGTT TATCGAAATC A 31

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCGCGGATCC ACCATGGAGG CGCTG 25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCGCTCTAGA TCAAGCGTAG TCTGGGACGT CGTATGGGTA ATTCAGTTTA TC 52

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys

```
1               5                   10                  15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
            20                  25                  30

Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
        35                  40                  45

Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
    50                  55                  60

Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65                  70                  75                  80

His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
                85                  90                  95

Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
            100                 105                 110

Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
        115                 120                 125

Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
    130                 135                 140

Asn Asp Pro Pro Cys Cys Arg Ser Val Asp Glu Thr Leu Arg Leu Val
145                 150                 155                 160

Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
                165                 170                 175

Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Pro Lys Thr Lys
            180                 185                 190

Glu Tyr Phe Ser Lys Gln Lys
        195
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met Ala Ser Gly Asn Ala Arg Ile Gly Lys Pro Ala Pro Asp Phe Lys
1               5                   10                  15

Ala Thr Ala Val Val Asp Gly Ala Phe Lys Glu Val Lys Leu Ser Asp
            20                  25                  30
```

```
Tyr Lys Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr
          35                  40                  45

Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asn Arg Ala Glu Asp
      50                  55                  60

Phe Arg Lys Leu Gly Cys Glu Val Leu Gly Val Ser Val Asp Ser Gln
65                  70                  75                  80

Phe Asn His Leu Ala Trp Ile Asn Thr Pro Arg Lys Glu Gly Gly Leu
                  85                  90                  95

Gly Pro Leu Asn Ile Pro Leu Leu Gly Asp Val Thr Arg Arg Leu Ser
             100                 105                 110

Glu Asp Tyr Gly Val Leu Lys Thr Asp Glu Gly Ile Ala Tyr Arg Gly
         115                 120                 125

Leu Phe Ile Ile Asp Gly Lys Gly Val Leu Arg Gln Ile Thr Val Asn
     130                 135                 140

Asp Leu Pro Val Gly Arg Ser Val Asp Glu Ala Leu Arg Leu Val Gln
145                 150                 155                 160

Ala Phe Gln Tyr Thr Asp Glu His Gly Glu Val Cys Pro Ala Gly Trp
                 165                 170                 175

Lys Pro Gly Ser Asp Thr Ile Lys Pro Asn Val Asp Asp Ser Lys Glu
             180                 185                 190

Tyr Phe Ser Lys His Asn
         195
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Met Ala Ala Ala Ala Gly Arg Leu Leu Trp Ser Ser Val Ala Arg Gly
1               5                  10                  15

Ala Ser Ala Ile Ser Arg Ser Ile Ser Ala Ser Thr Val Leu Arg Pro
            20                  25                  30

Val Ala Ser Arg Arg Thr Cys Leu Thr Asp Ile Leu Trp Ser Ala Ser
        35                  40                  45

Ala Gln Gly Lys Ser Ala Phe Ser Thr Ser Ser Ser Phe His Thr Pro
    50                  55                  60
```

Ala Val Thr Gln His Ala Pro Tyr Phe Lys Gly Thr Ala Val Val Asn
65 70 75 80

Gly Glu Phe Lys Glu Leu Ser Leu Asp Asp Phe Lys Gly Lys Tyr Leu
85 90 95

Val Leu Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys Pro Thr Glu
100 105 110

Ile Val Ala Phe Ser Asp Lys Ala Asn Glu Phe His Asp Val Asn Cys
115 120 125

Glu Val Val Ala Val Ser Val Asp Ser His Phe Ser His Leu Ala Trp
130 135 140

Ile Asn Thr Pro Arg Lys Asn Gly Gly Leu Gly His Met Asn Ile Thr
145 150 155 160

Leu Leu Ser Asp Ile Thr Lys Gln Ile Ser Arg Asp Tyr Gly Val Leu
165 170 175

Leu Glu Ser Ala Gly Ile Ala Leu Arg Gly Leu Phe Ile Ile Asp Pro
180 185 190

Asn Gly Val Val Lys His Leu Ser Val Asn Asp Leu Pro Val Gly Arg
195 200 205

Ser Val Glu Glu Thr Leu Arg Leu Val Lys Ala Phe Gln Phe Val Glu
210 215 220

Thr His Gly Glu Val Cys Pro Ala Asn Trp Thr Pro Glu Ser Pro Thr
225 230 235 240

Ile Lys Pro Ser Pro Thr Ala Ser Lys Glu Tyr Phe Glu Lys Val His
245 250 255

Gln

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ser Ser Gly Asn Ala Lys Ile Gly Tyr Pro Ala Pro Asn Phe Lys
1 5 10 15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser

```
            20                  25                  30

Glu Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
        35                  40                  45

Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Asp
    50                  55                  60

Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65                  70                  75                  80

His Phe Cys His Leu Ala Trp Ile Asn Thr Pro Lys Lys Gln Gly Gly
                85                  90                  95

Leu Gly Pro Met Asn Ile Pro Leu Ile Ser Asp Pro Lys Arg Thr Ile
            100                 105                 110

Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
        115                 120                 125

Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Ile
    130                 135                 140

Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Ile Ile Arg Leu Val
145                 150                 155                 160

Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
                165                 170                 175

Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Asn Lys Ser Lys
            180                 185                 190

Glu Tyr Phe Ser Lys Gln Lys
        195
```